

FIGURE 1

HKLK2.LA0	(6998)	AA-CTGAGCCTTGATTATATTG-GAGCTTGGTTGCA-CAG-ACATGTCGA
PSE	(509)	AATCT-AG-C-TGA-TATAGTGTG-GCTCAAAACCTTCAGCACAAATC-A
HKLK2.LA0	(7044)	CCACCTTCATGGCTGAACTTTAGTACTTAGCCCCCTCCAGACGTCTACAGC
PSE	(553)	-CACCGTTA-GACT--A-TCTGGT--GT-G--GC-CCAAAC--CTTCAGG
HKLK2.LA0	(7094)	TGATAGGCTGTAACCCAACAT-TGTCACCATAAATCACATTGTTAGACTA
PSE	(590)	TGA-ACAAAGGGACTCTA-ATCTGGCAGGAT-ATTC-CA----AAG-C-A
HKLK2.LA0	(7143)	TCCAGTG-TGGCC-CAAGCTCCCGTGTAACACAGGCACTCTAAACAG--
PSE	(630)	T-TAGAGATGACCTCTTGC-AAAG-AAAAAGAAATGGAAAAGAAAAAGAA
HKLK2.LA0	(7189)	-G-CAGGATATTTCAAAAGCTT-AGAGATGACCTCCCAGGAGCTGAATGC
PSE	(677)	AGAAAGGAAAAAAAAAAAAAAAAAGAGATGACCTCTCAGGCTCTGAGGGG
HKLK2.LA0	(7236)	AAA-GACCTGGCCTCTTTGGGCAAGGAGAATCCTTTACCGCACACTCTCC
PSE	(727)	AAACG-CCTGAGGTCTTTGAGCAAGGTCAGTCCTCTGTTGCACAGTCTCC
HKLK2.LA0	(7285)	TTCACAGGGTTATTGTGAGGATCAAATGTGGTCATGTGTGTGAGACACCA
PSE	(776)	CTCACAGGGTCATTGTGACGATCAAATGTGGTCACGTGTATGAGGCACCA
HKLK2.LA0	(7335)	GCACATGCTCTGGCTGTGGAGAGTGACTTCTA--TGTTGTCTAACATTGCT
PSE	(826)	GCACATGCCTGGCTCTGGGGAGTGCCGTGTAAGTGTATGCTTGCACCTGCT
HKLK2.LA0	(7383)	GAGTGCTAAGAAAGTATTAGGCATGGCT-TTCAGCACATCAGATGCTCA
PSE	(876)	GAATGCTTGGGATGIGTCAGGGAT-TATCTTCAGCACATCAGATGCTCA

FIGURE 2A

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HKLK2.LA0	(7432)	TCTAATCCTCACAACATGGCTACAGGG-TGGGCACTACTAGCCTCATTG
PSE	(925)	TCTCATCCTCACAGCATCACTA-TGGGATGGGTATTACTGGCCTCATTG
HKLK2.LA0	(7481)	ACAGAGGAAAG-GACTGTGGATAAGAAGGGGGTGACCAATAGGTCAGAGT
PSE	(974)	ATGGA-GAAAGTGGCTGTGGCTCAGAAAGGGGGGACCACTAGACCAGGGA
HKLK2.LA0	(7530)	CATTCTGGATGCAAGGGG-CTCCAGAGGACCATGATTAGACATTGTCTGC
PSE	(1023)	CACTCTGGATGC-TGGGGACTCCAGA-GACCATGACCACTACCAACTGC
HKLK2.LA0	(7579)	AGAGAAATT----ATGG-CTGGATGTCTCTGCCCGGAAAGGG-GGA--T
PSE	(1071)	AGAGAAATTAATTGTGGCCT-GATGTCCCTGTCTTGAGAGGGTGGAGGT
HKLK2.LA0	(7621)	GCACTTTCTTGACCCCTATCTCAGATCTTGACTTTGAG-GTTATCTCA
PSE	(1120)	GGACCTTCACTAACCTCCTACCT-TGACCCTCTCTTTAGGGCTCTTCT
HKLK2.LA0	(7670)	GACTTCCTCTATGATACCAGGAGCCCATCATAATCTCTCTGTGTCTCTC
PSE	(1169)	GACCTCCACCATGGTACTAGGA-CCC--CATTGTAT-TCTGT-ACC-CT-
HKLK2.LA0	(7720)	CCCTTCCTCAGTCTTACTG-CCCACTCTTCCAGCTCCATCTCCAGCTGG
PSE	(1212)	--C-T--TGACTC-TA-TGACCCCCACTGCCCA-CTGCA--TCCAGCT--
HKLK2.LA0	(7769)	CCAGGTGTAGCCACAGTACCTAACTCT-TTGCAGAGAACTATAAATGTGT
PSE	(1250)	---GG-GT--CC-C-CT-CCTATCTCTATT-CCCAG--CTGGCCA-GTGC
HKLK2.LA0	(7818)	A-TCCTACAGGGGAGAAAAAAA-AAAAG-AACTCTGAAAGAGCTGACATT
PSE	(1287)	AGT-CT-CAGTGCCACCTGTTTGTGAGTAAGTCTGAAGGGGCTGACATT
HKLK2.LA0	(7865)	TTACCGACTTGCAAACACATAAGCTAACCTGCCAG--TTTTGT----GCT
PSE	(1335)	TTACTGACTTGCAAACAAATAAGCTAACITTCAGAGTTTTGTGAATGCT
HKLK2.LA0	(7909)	GGTAGAACT-CATGAGACTCCTGGGTGAGAGGCAAAAGATTTTATTACCC
PSE	(1385)	GGCAG-AGTCCATGAGACTCCTGAGTCAGAGGCAAAAGGCTTTTACTGCTC

FIGURE 2B

HKLK2.LA0	(7958)	ACAGCTAAGGAGGCAGCATGAACTTTGTGTTACATTTGTTCACTTTGCC
PSE	(1434)	ACAGCTTAGCAGACAGCATGAGGTTTCATGTTACATTAGTACACCTTGCC
HKLK2.LA0	(8008)	CCCC--AATTCATAT-GGGATGATCAGAGCAGTTC-AGGTGGATG--G-A
PSE	(1484)	CCCCCAAATCTTGTAGGG-TGACCAGAGCAG-TCTAGGTGGATGCTGTG
HKLK2.LA0	(8051)	CA-CAGGGGTTTGTGGCAAAGGTGAGCAACCTAG-GCTTAGAAATCCTCA
PSE	(1532)	CAGAAGGGGTTTGTGCCACTGGTGAGAAACCT-GAGATTAGGAATCCTCA
HKLK2.LA0	(8099)	ATCTTATAAGAAGGTACT---AGCAAACCTTGTC-CAGTCTTTGTATCTGA
PSE	(1581)	ATCTTAT-ACTGGG-ACAACCTTGCAAACCTG-CTCAGCCTTTGTCTCTGA
HKLK2.LA0	(8145)	CGGAGATATTATCTTTATAAT-TGGG-TTGAAAGCAGACCTACTCTGGAG
PSE	(1628)	TGAAGATATTATCTTCATGATCTTGGATTGAAAACAGACCTACTCTGGAG
HKLK2.LA0	(8193)	GAACATATTGTATTTATTGTCTT-GAACAGTAAACAAATCTGCTGTAAAA
PSE	(1678)	GAACATATTGTATCGATTGTCTTG-ACAGTAAACAAATCTGTTGT--AA
HKLK2.LA0	(8242)	TAGACGTAACTTTATTATCTAAGG-CAGTAAGCAAACCTAGATCTGAAG
PSE	(1725)	GAGACATTATCTTTATTATCT-AGGACAGTAAGCAAGCCTGGATCTG-AG
HKLK2.LA0	(8291)	-GCGATACCATCTTGCAAGGCTATCTGCTGTACAAATATGCTTGAAAAGA
PSE	(1773)	AGAGATATCATCTTGCAAGGATGCCTGCTTTACAAACATCCTTGAAACAA
HKLK2.LA0	(8340)	TGGTCCAGAAAAGAAAACGGTATTATTGCCTTTGCTCAGAAGACACACAG
PSE	(1823)	CAATCCAGAAAA-AAAAAGGIGTTGCTGTCTTTGCTCAGAAGACACACAG
HKLK2.LA0	(8390)	AAACATAAGAGAACCATGGAAAATTGTCTCCCAACACTGTTACCCAGAG
PSE	(1872)	ATACGTGACAGAACCATGGAGAATTGCCTCCCAACGCTGTTACGCCAGAG
HKLK2.LA0	(8440)	CCTTCCACTCTTGTCTGCAGCACAGTCTTAACATCCCATCAITAG-T-GT
PSE	(1922)	CCTTCCACCCTTGTCTGCAGCACAGTCTTAACGTTCCACCAITAAATACT

FIGURE 2C

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HKLK2.LA0	(8488)	--GTCTACCACATCTGGCTTCACCGTGCCTAACCAAGATTTCTAGGTCCA
PSE	(1972)	TCTTCTATCACATCCTGCTTCTTTATGCCTAACCAAG-GTTCTAGGTCCC
HKLK2.LA0	(8536)	GTTCCCCACCATGTTTGGCAGTGCCTTACTGCCAACCCCAAGGGA
PSE	(2021)	GAT--CGACTGCTGTGGCAGCACTCCACTGCCAAACCCAGAATAAGGCA
HKLK2.LA0	(8586)	GTGCTCAGAAATTCCTGA
PSE	(2069)	GCGCTCAGGATCCCCGA

FIGURE 2D

09/875,228-102301

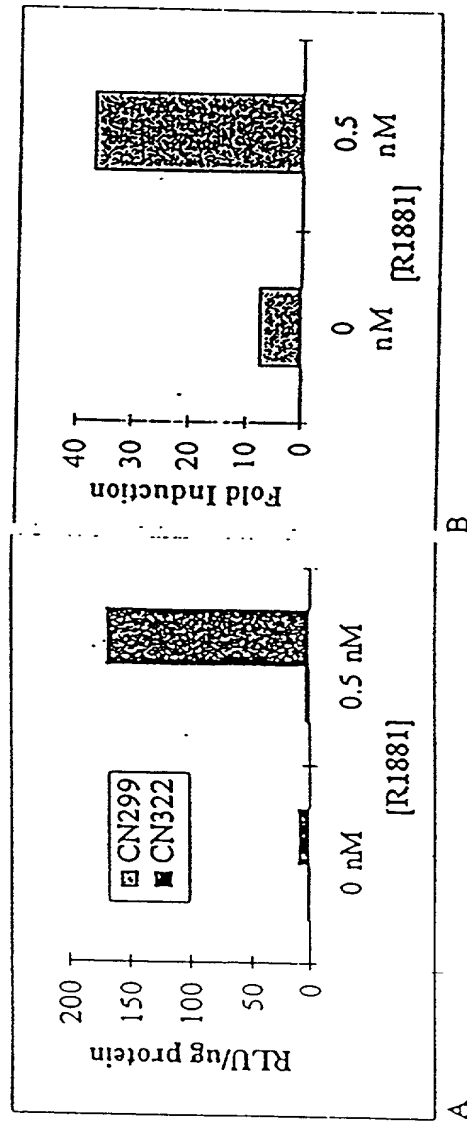


FIGURE 3

FIGURE 3

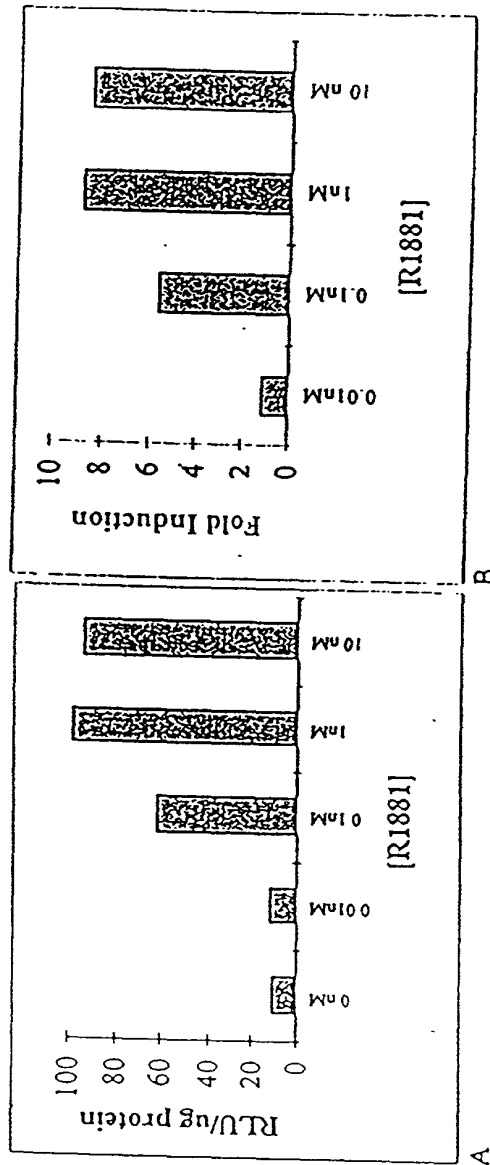


FIGURE 4

FIGURE 4

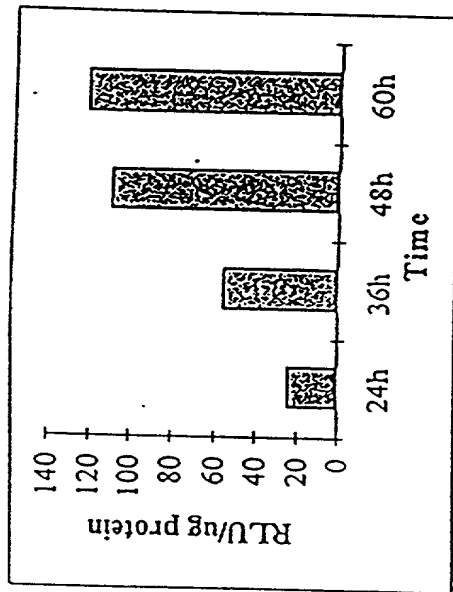


FIGURE 5

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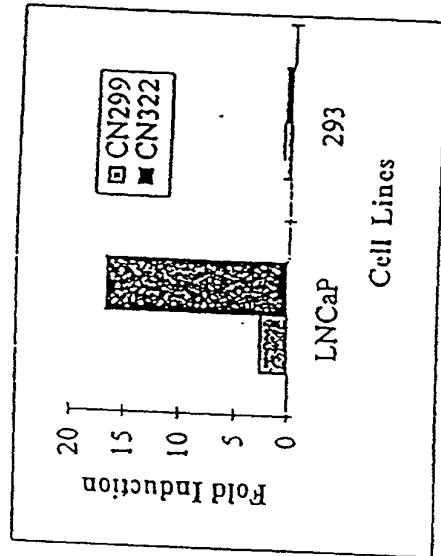


FIGURE 6

FIGURE 6

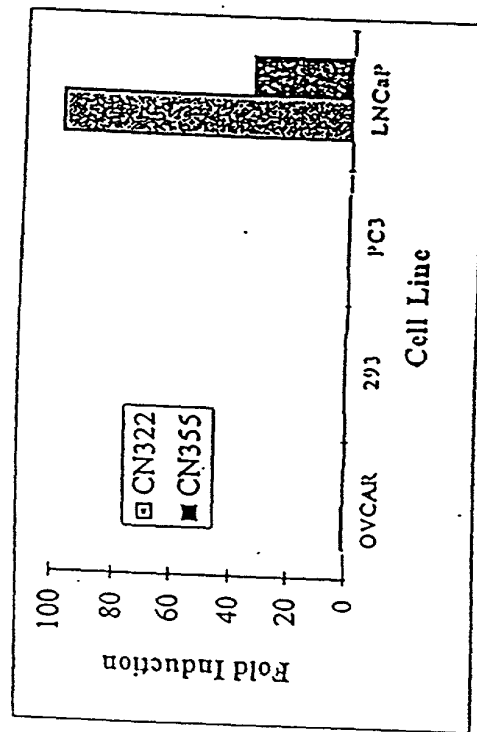


FIGURE 7

FIGURE 7

			Fold Induction
CN379	-5155	-3387	-324
			81
CN386		-3529	
			50
CN387		-3643	
			90
CN388	-4814	-3387	
			35
CN389		-3529	
			30
CN390		-3643	
			96
CN391	-4457	-3387	
			61
CN392		-3529	
			53
CN393		-3643	
			30
CN394		-3993	-3387
			55
CN395		-3529	
			45
CN396		-3643	
			37

FIGURE 8

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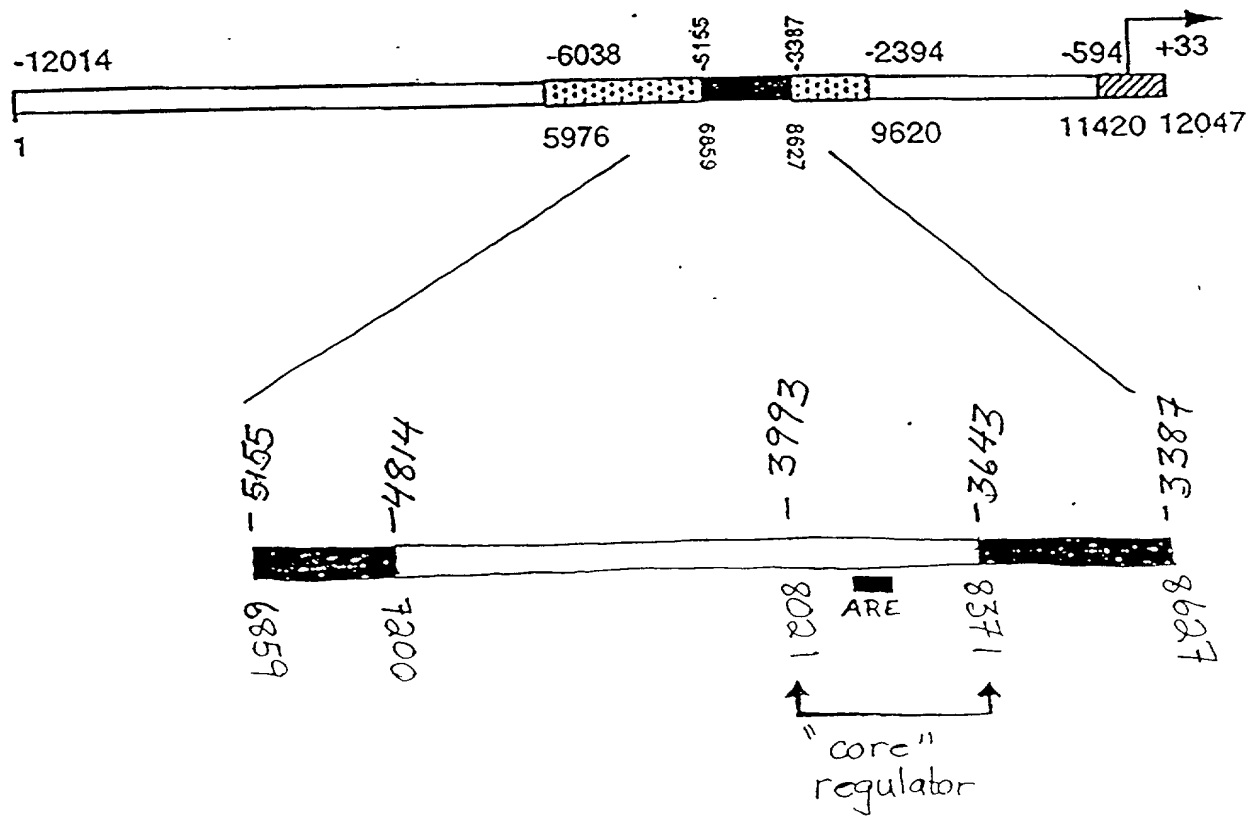
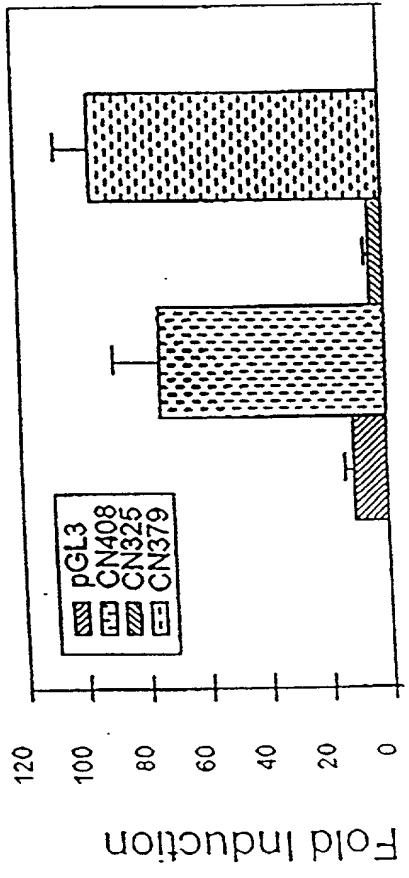


FIGURE 9

A



Constructs

B

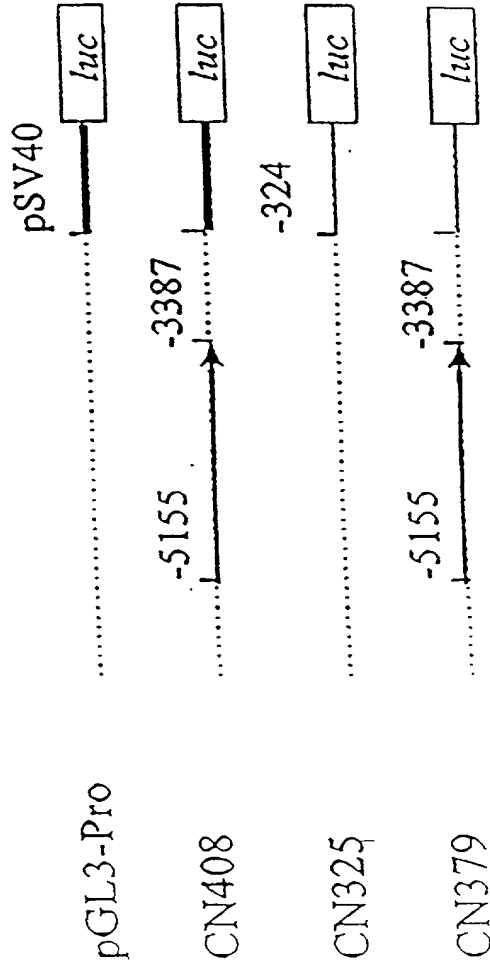


FIGURE 10

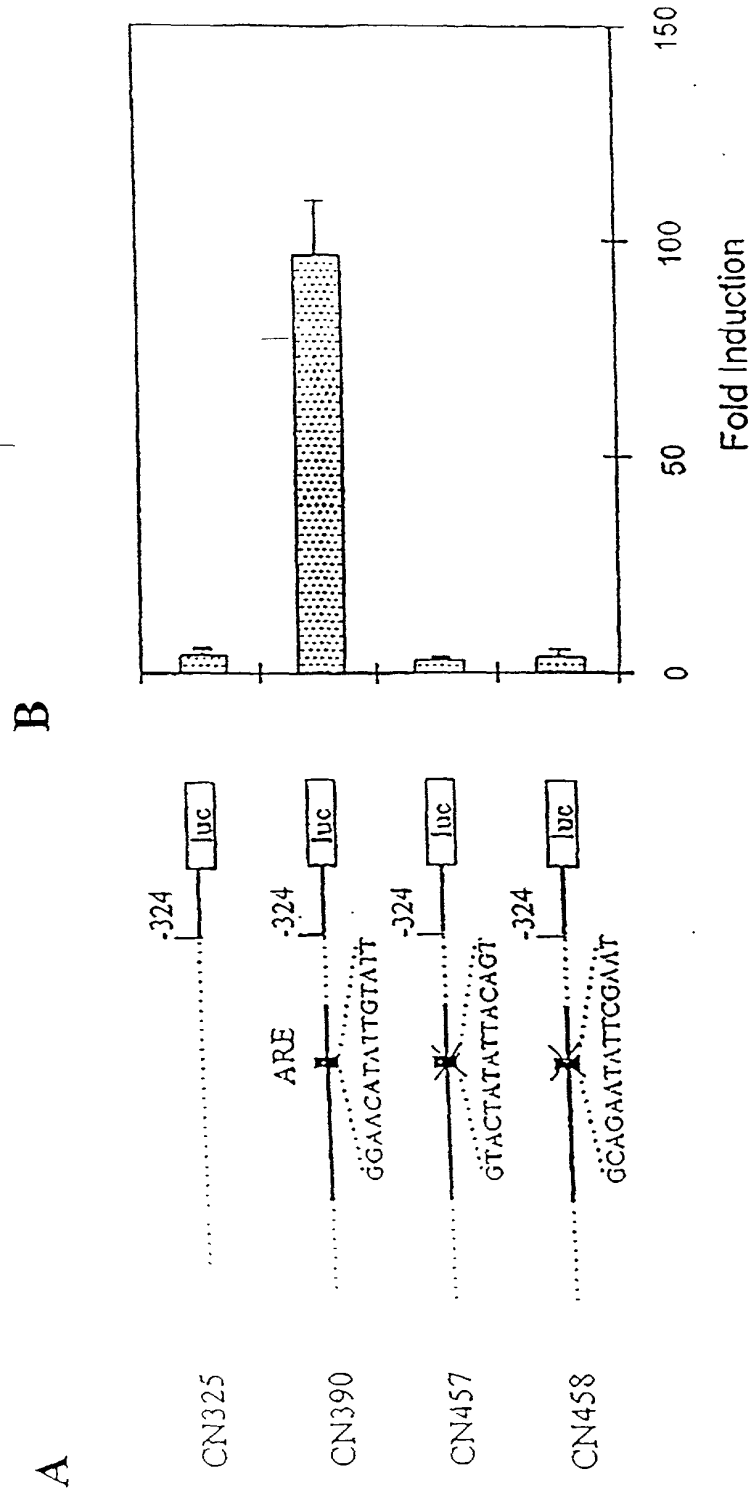


FIGURE 11

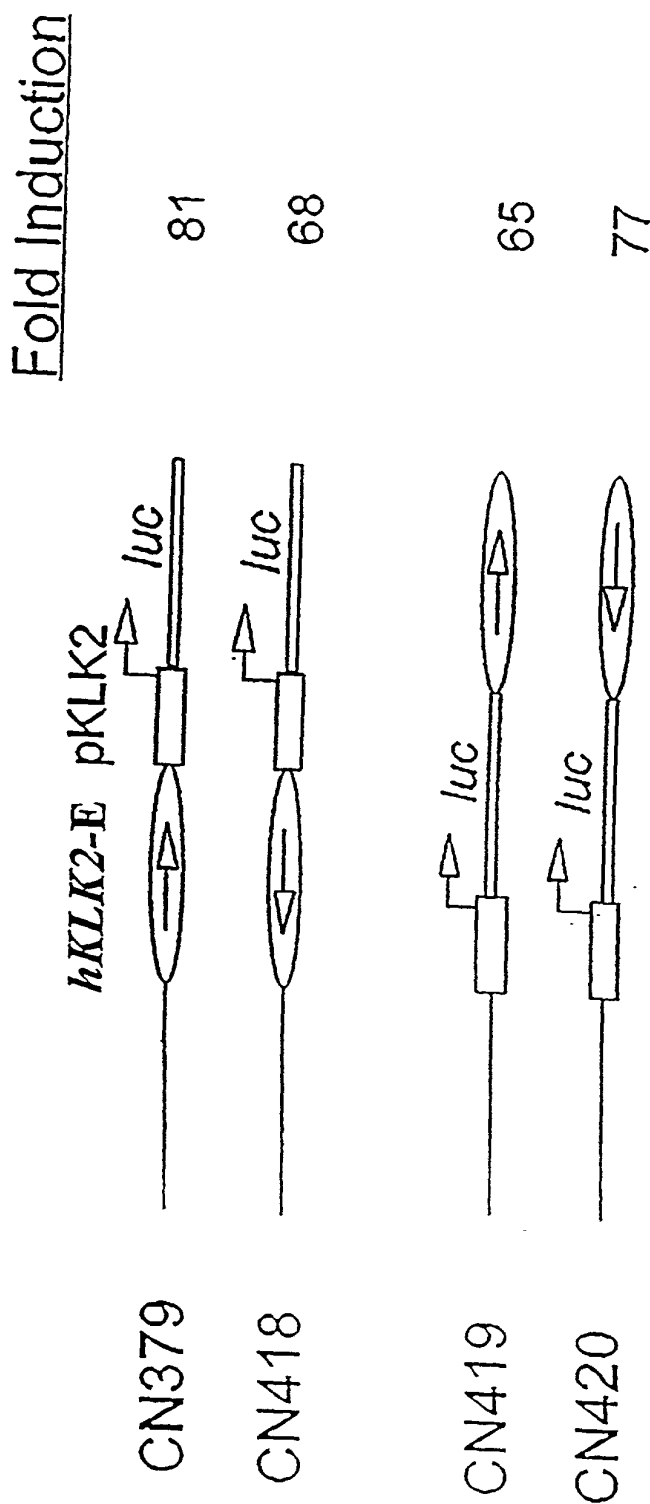


FIGURE 12

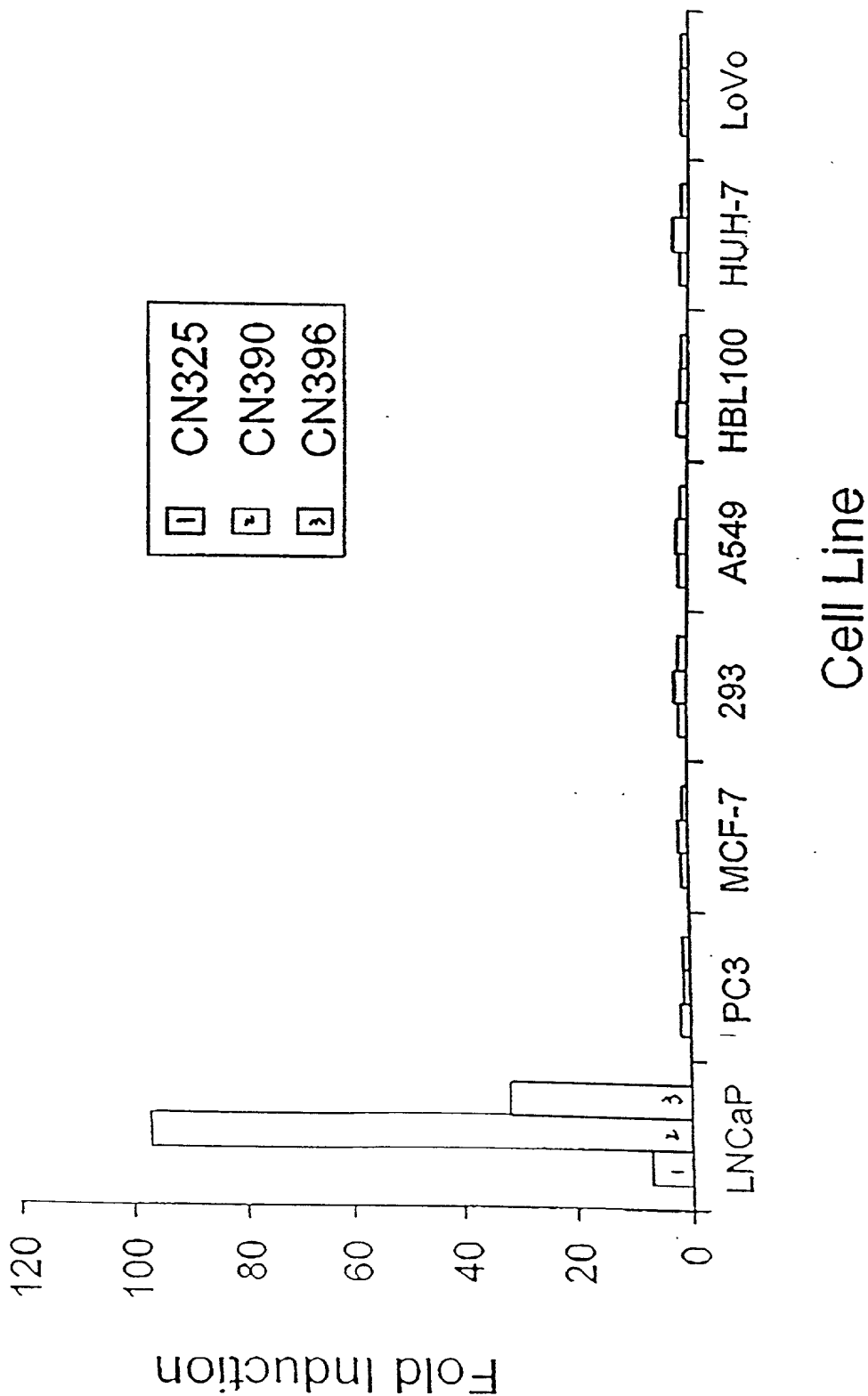


FIGURE 13

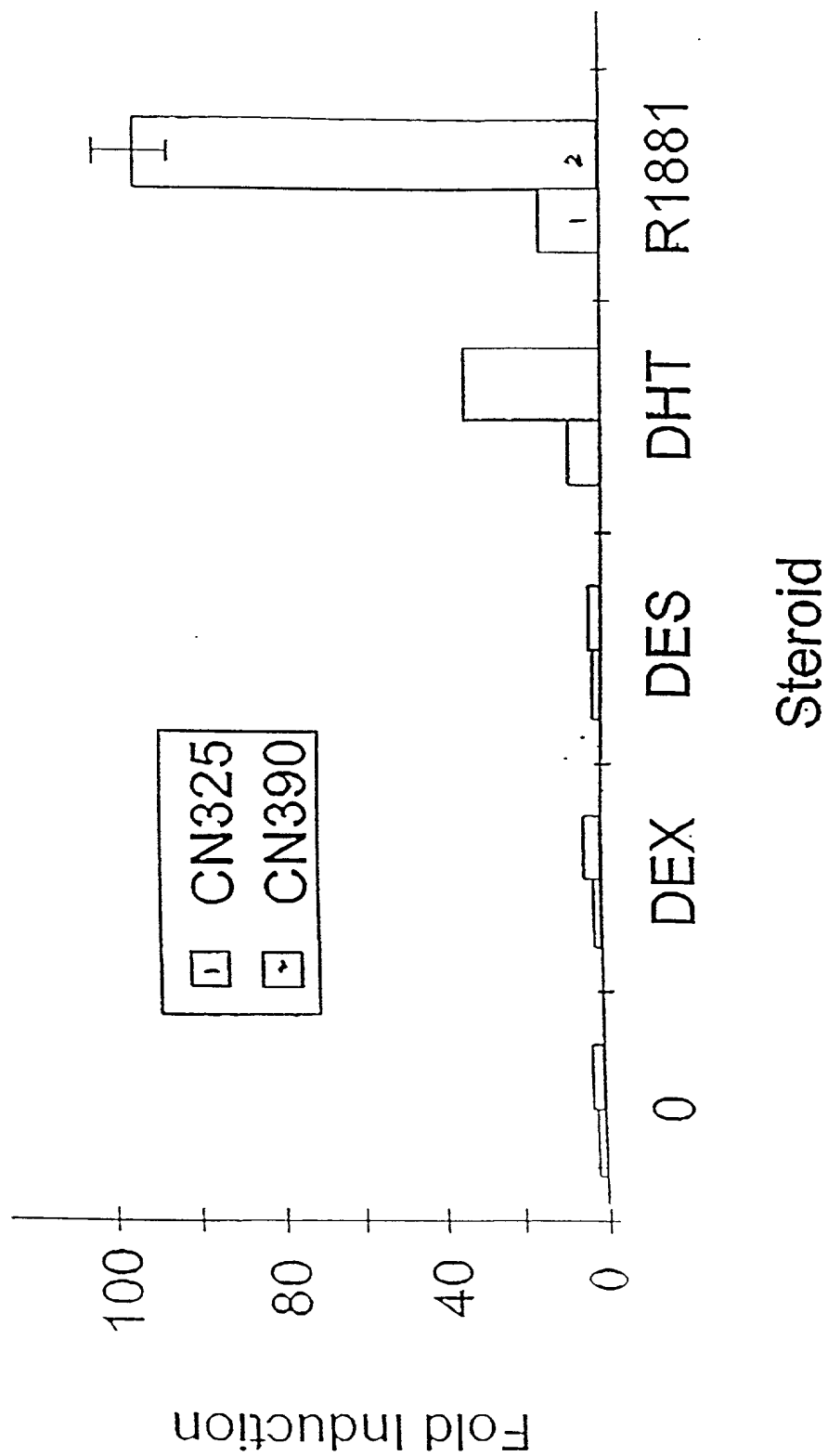


FIGURE 14

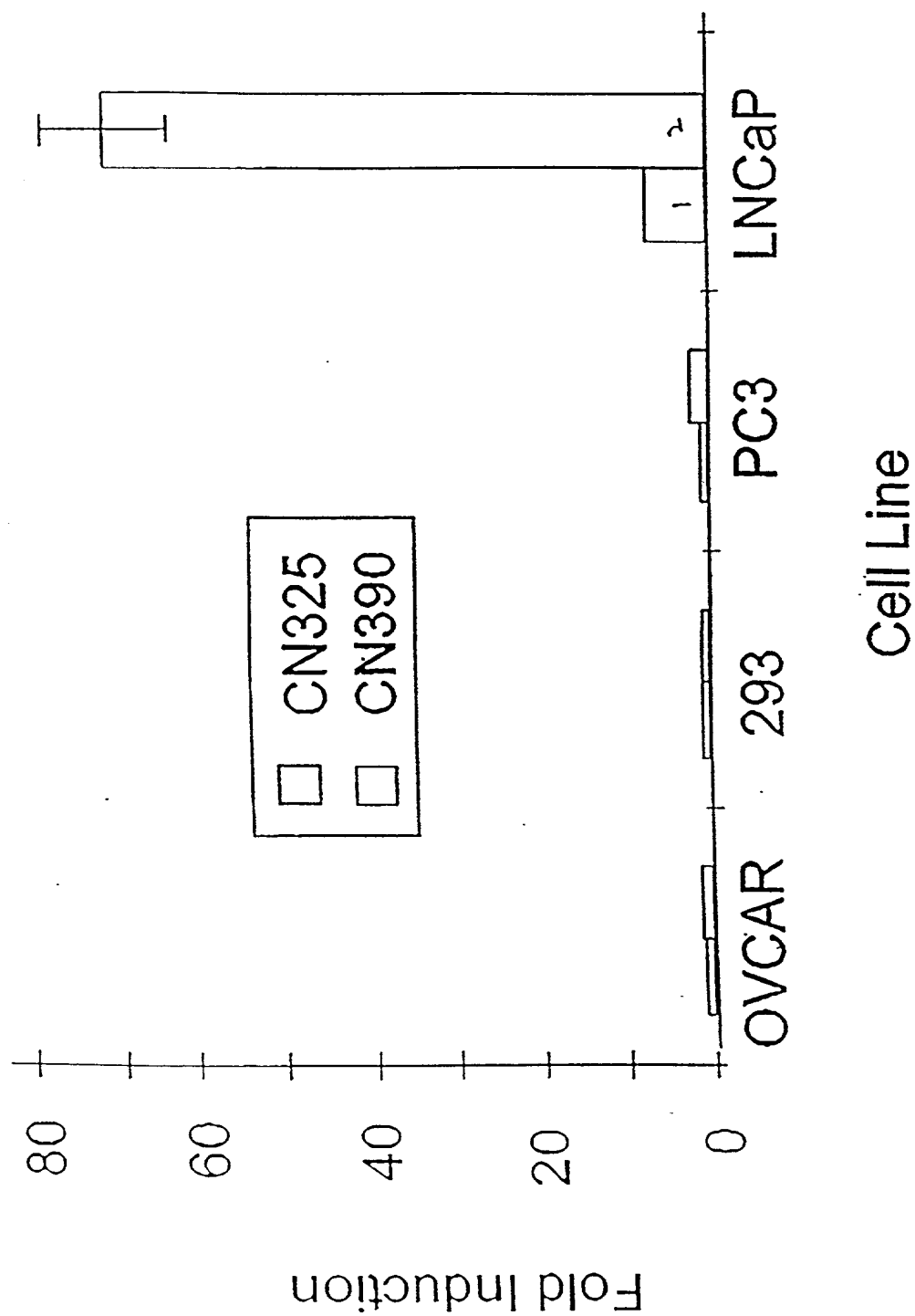


FIGURE 15

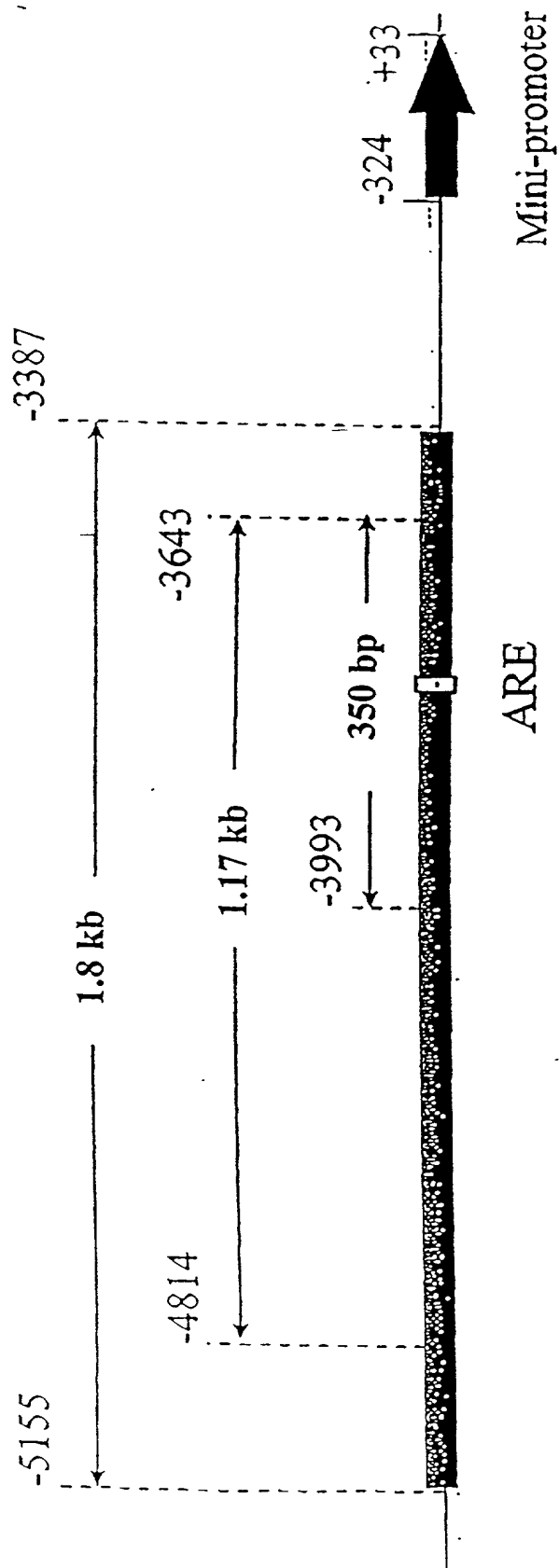


FIGURE 16

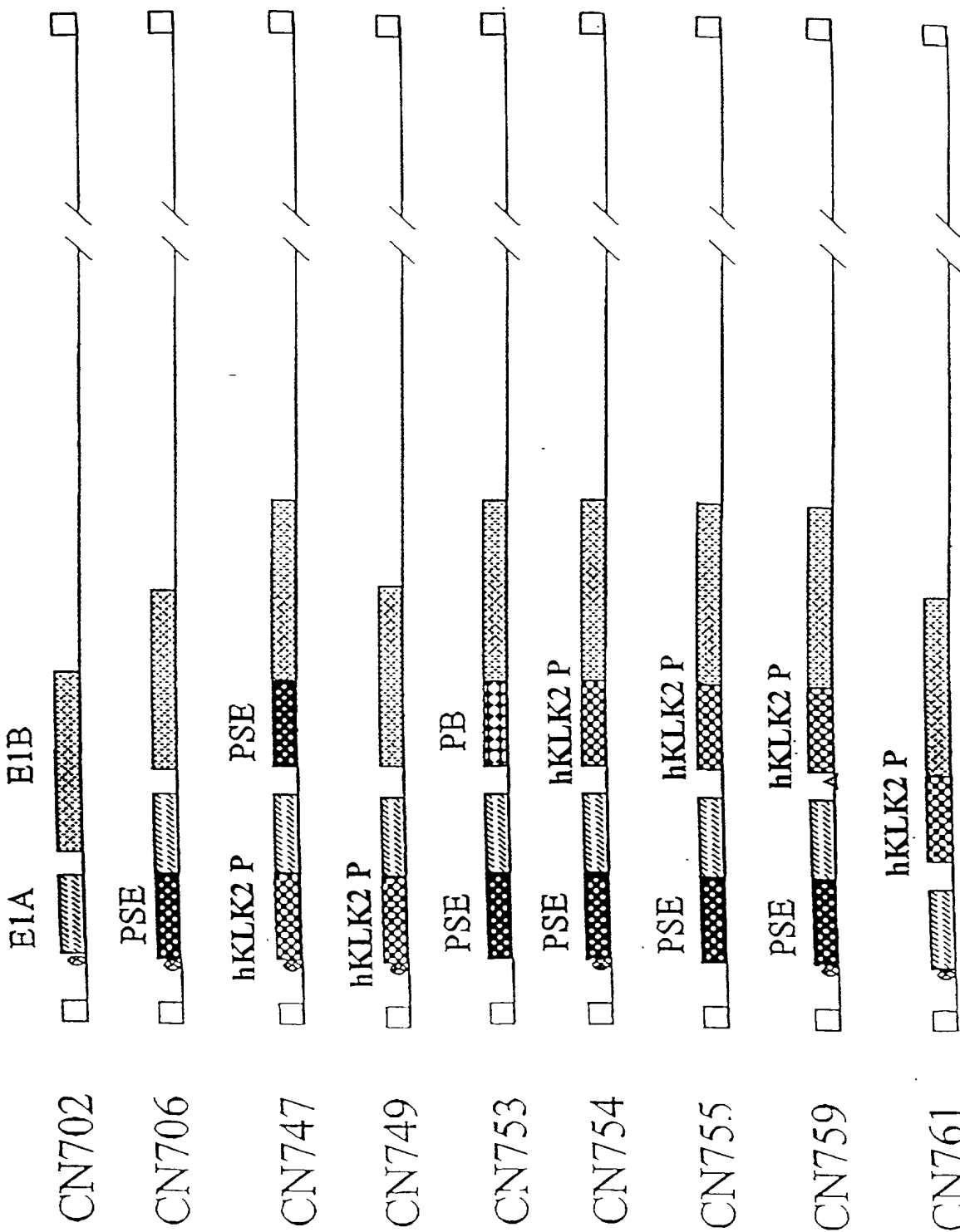
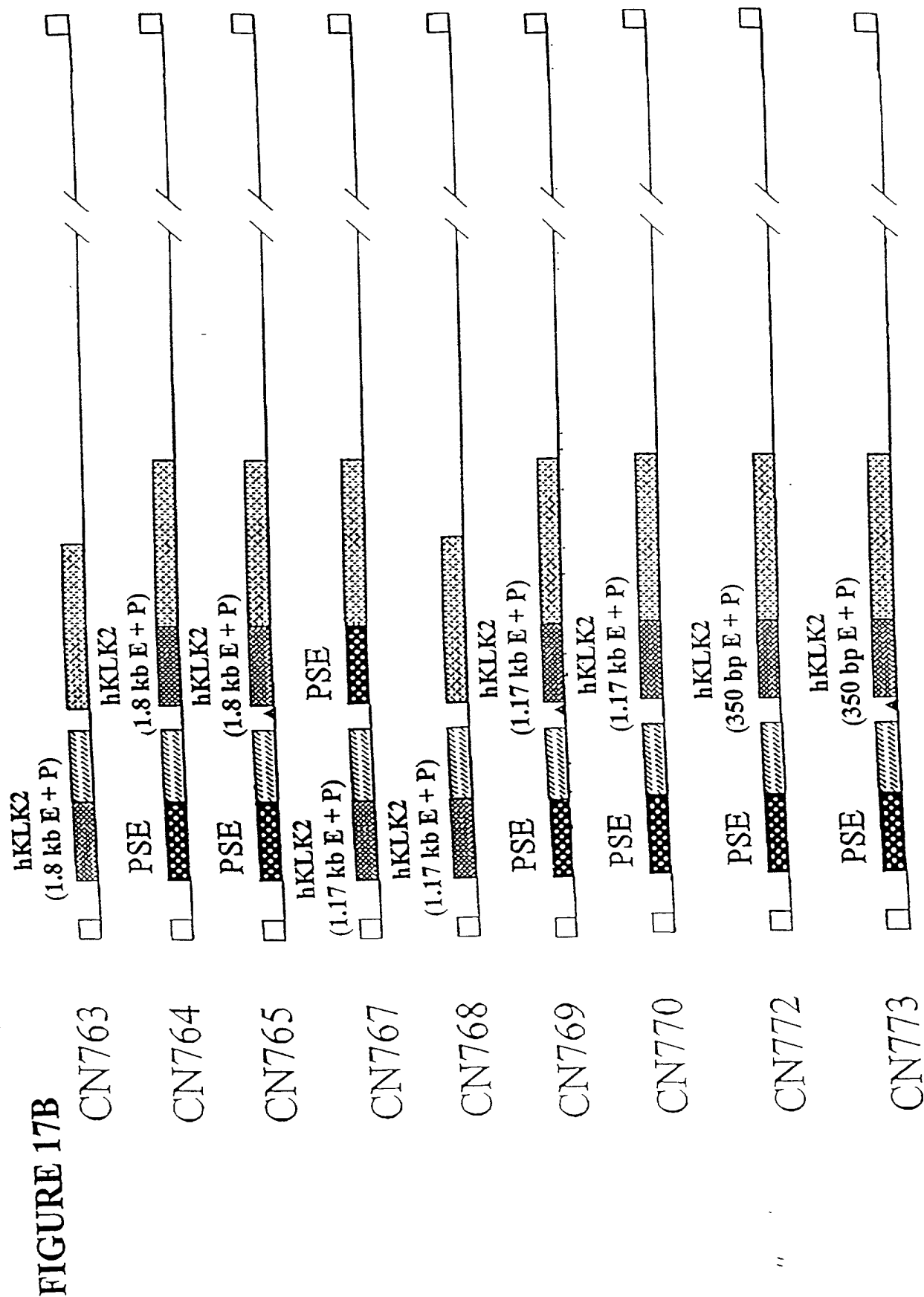


FIGURE 17A



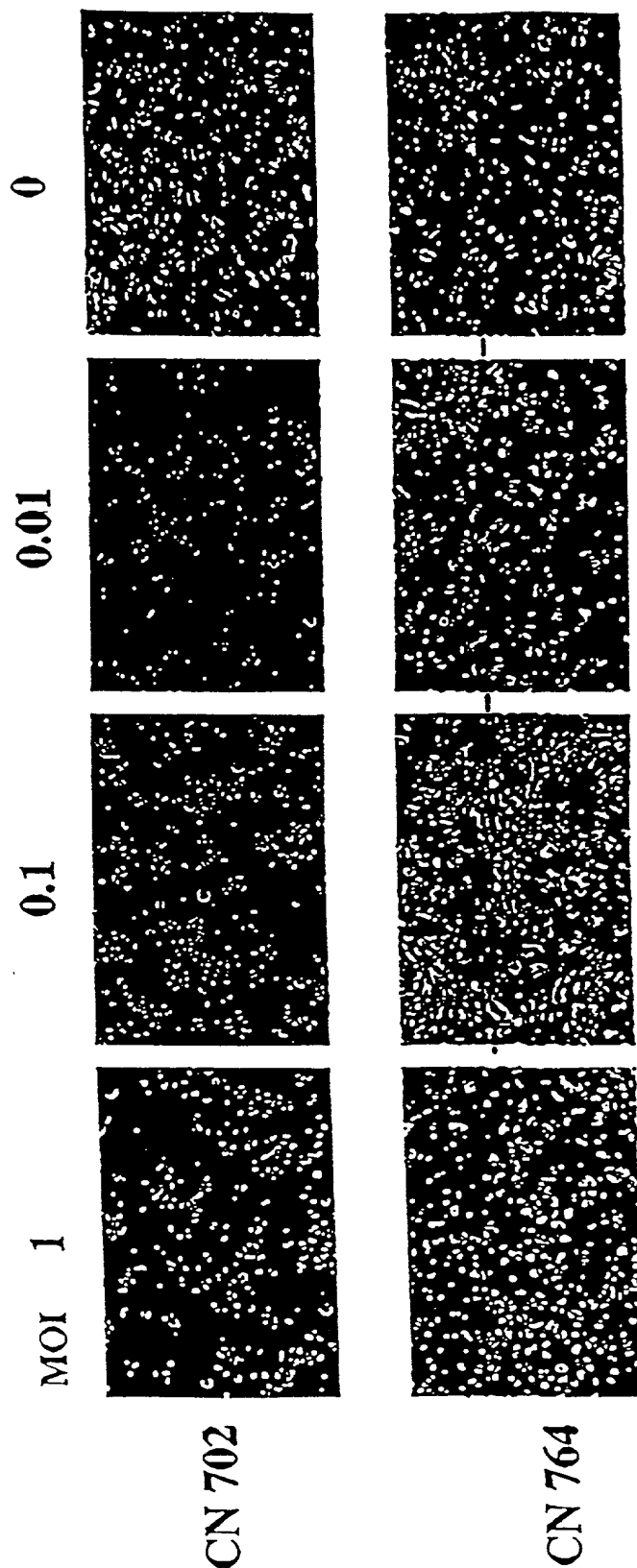


FIGURE 18

FIGURE 18

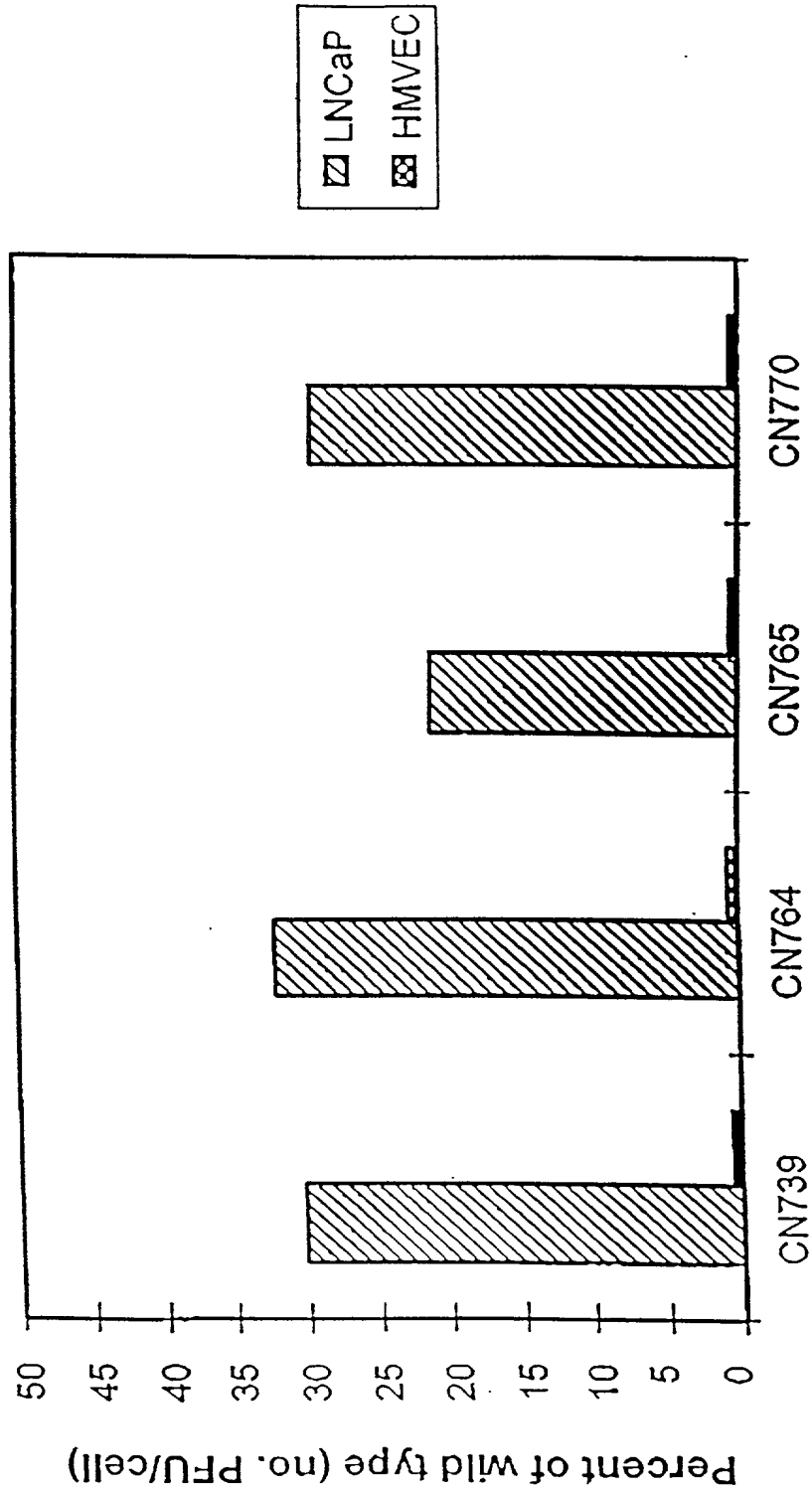


FIGURE 19

FIGURE 19

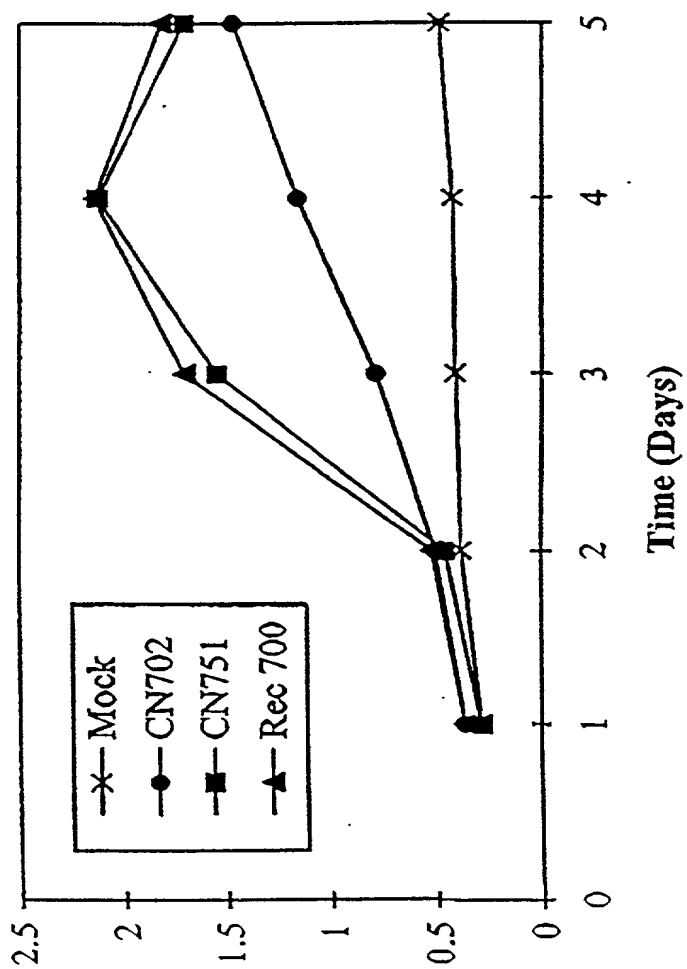


FIGURE 20

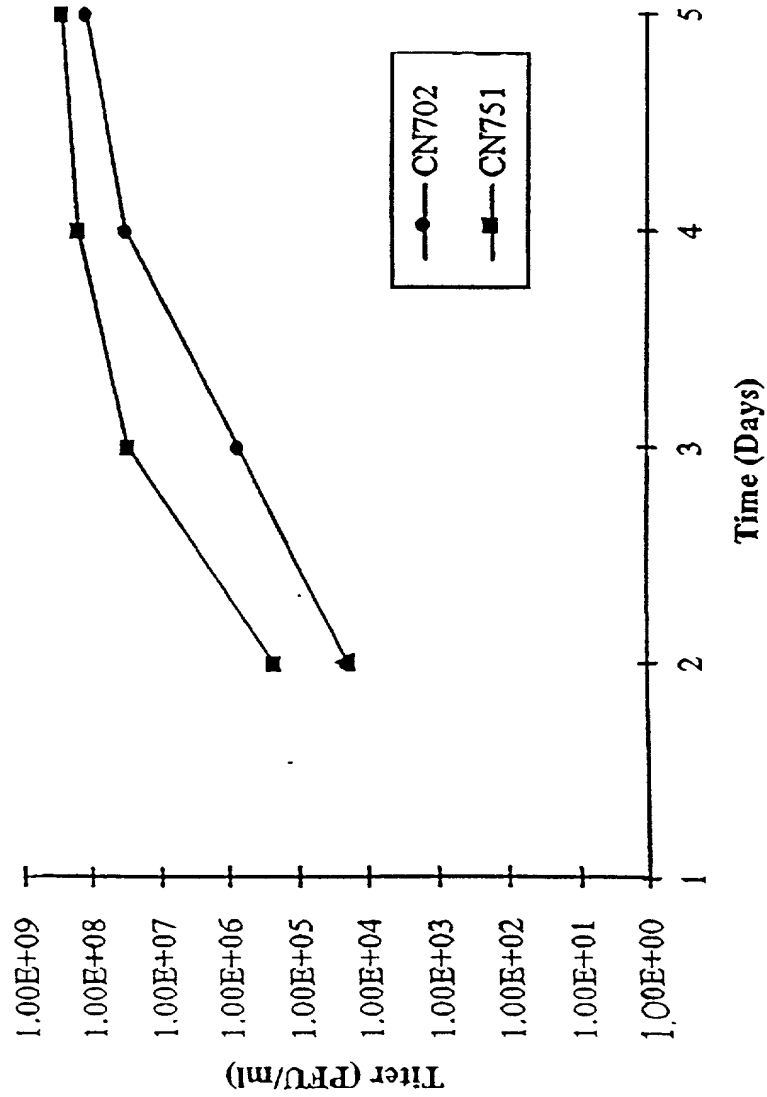


FIGURE 21

FIGURE 21

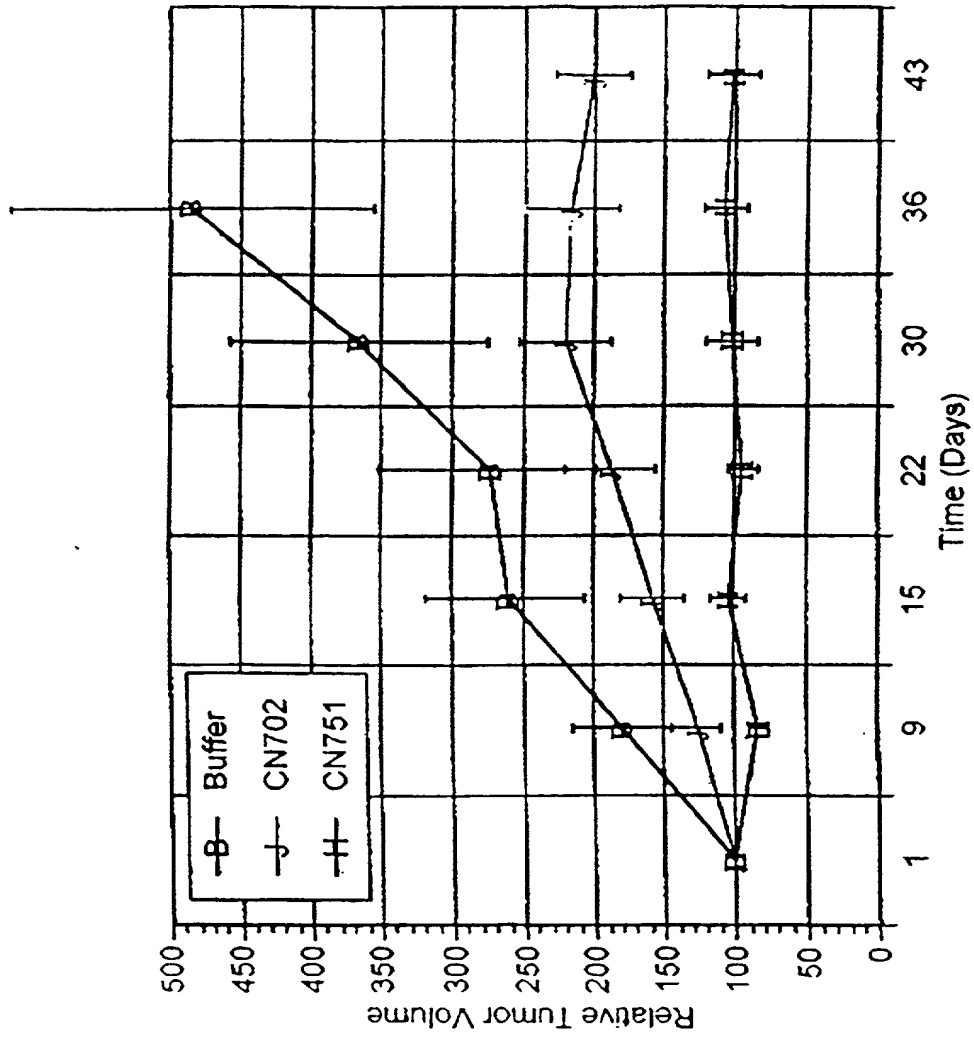


FIGURE 22

FIGURE 22

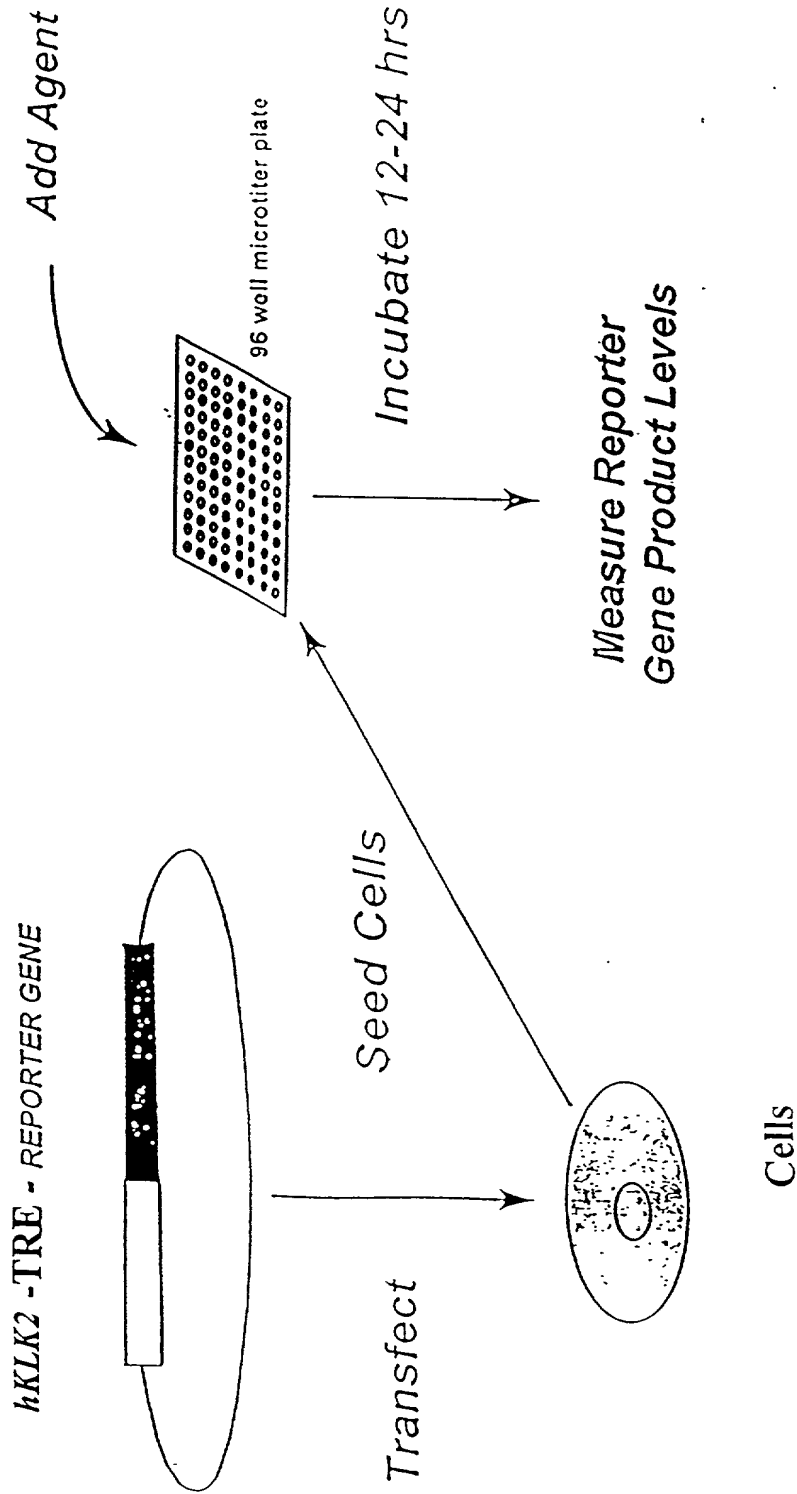
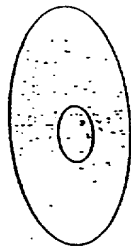


FIGURE 23A

FIGURE 23A



Cells

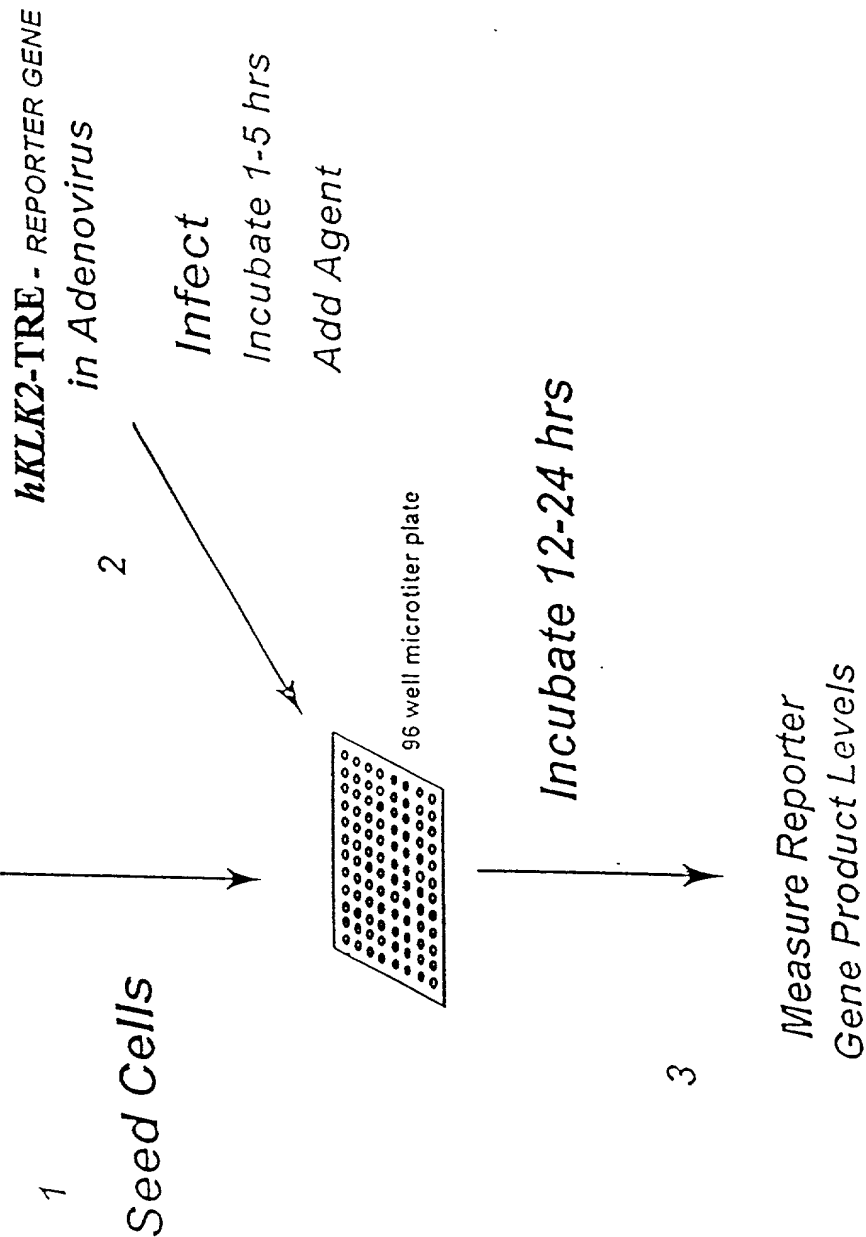


FIGURE 23B

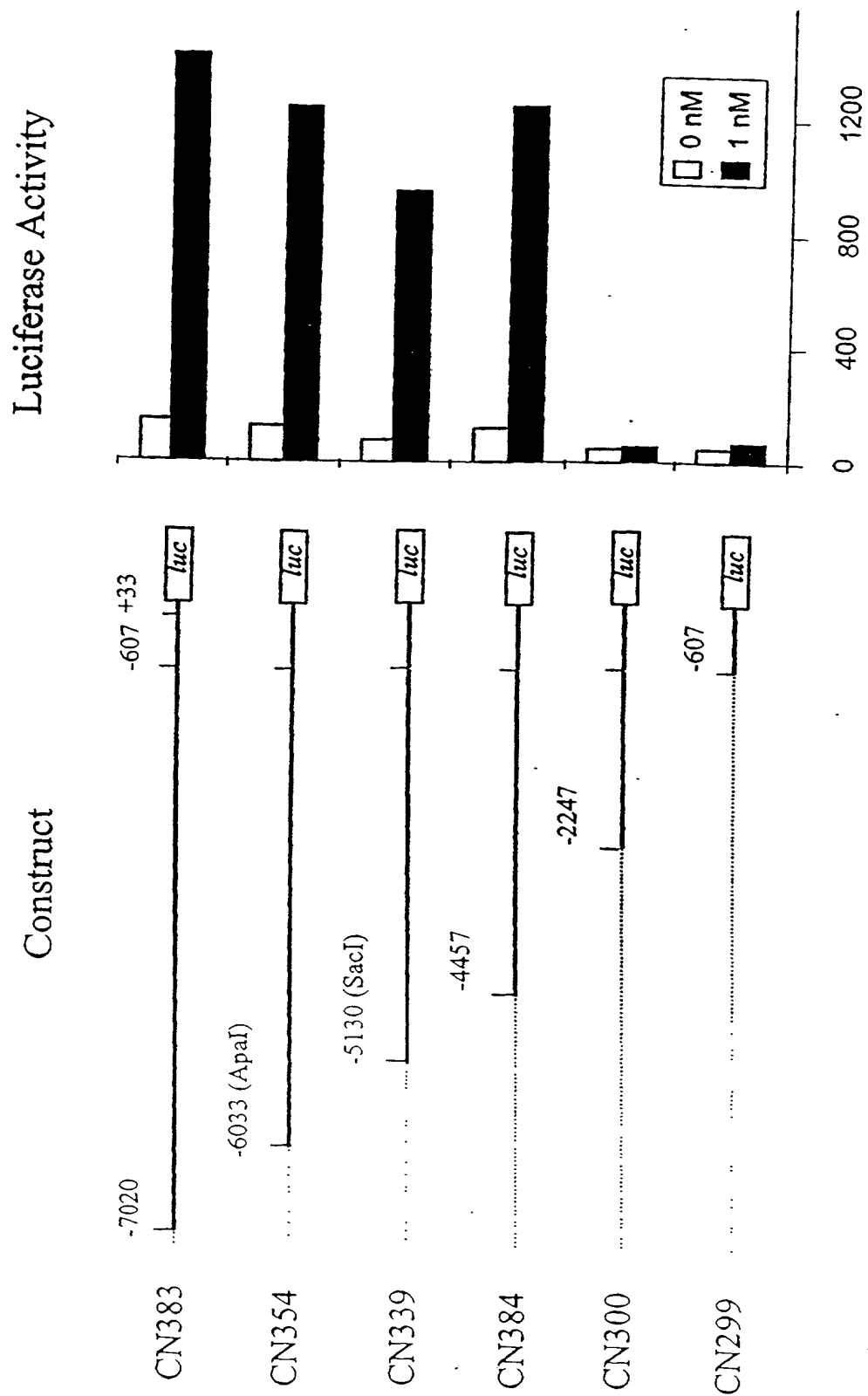
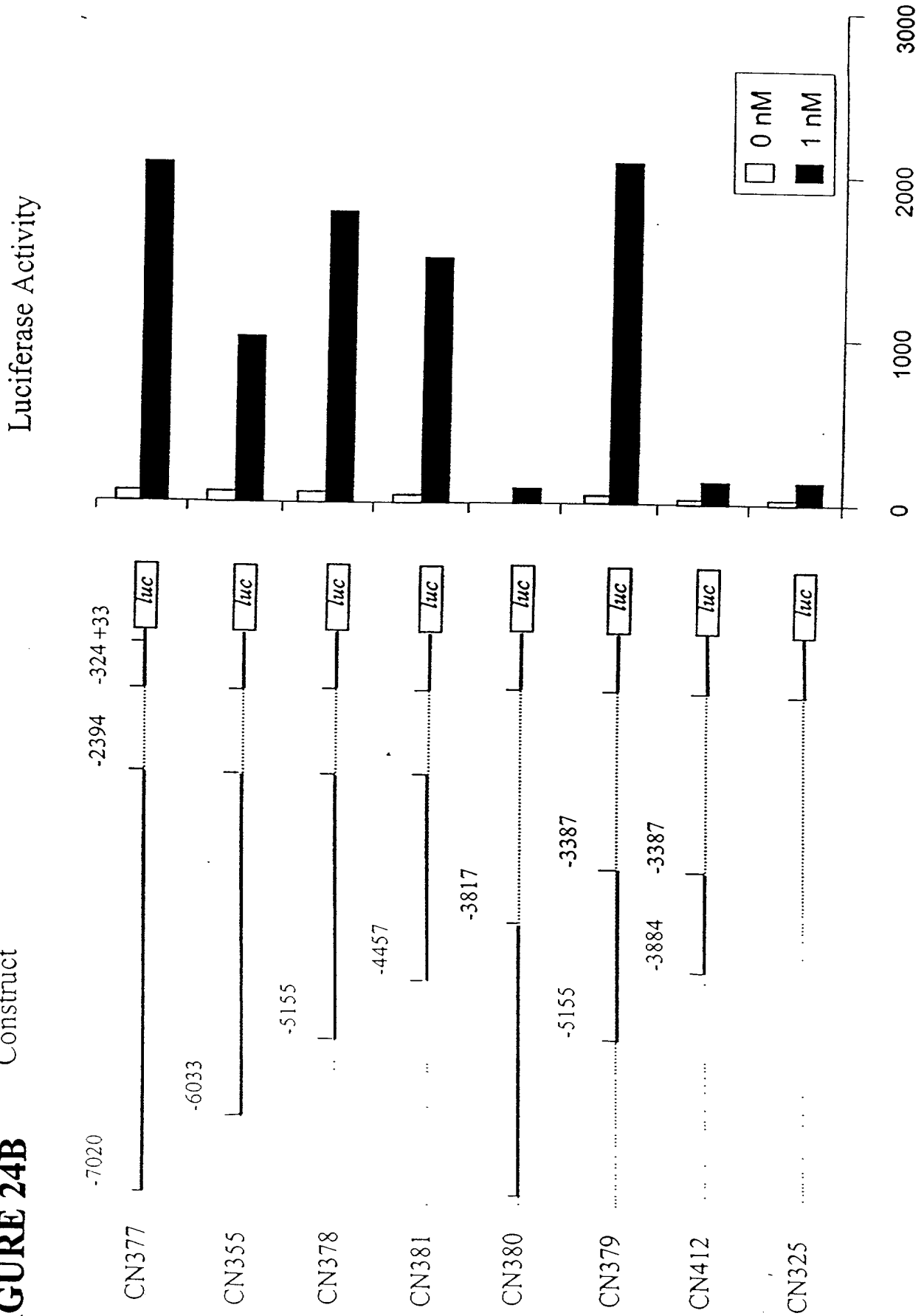


FIGURE 24A

FIGURE 24B Construct



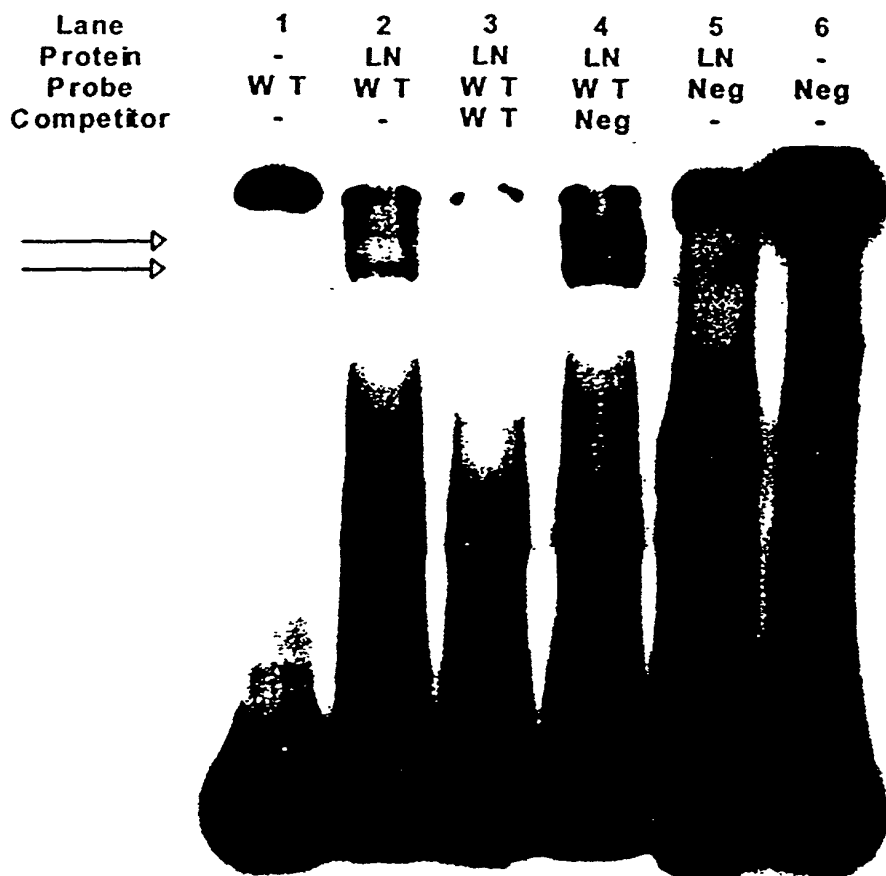


FIGURE 25A

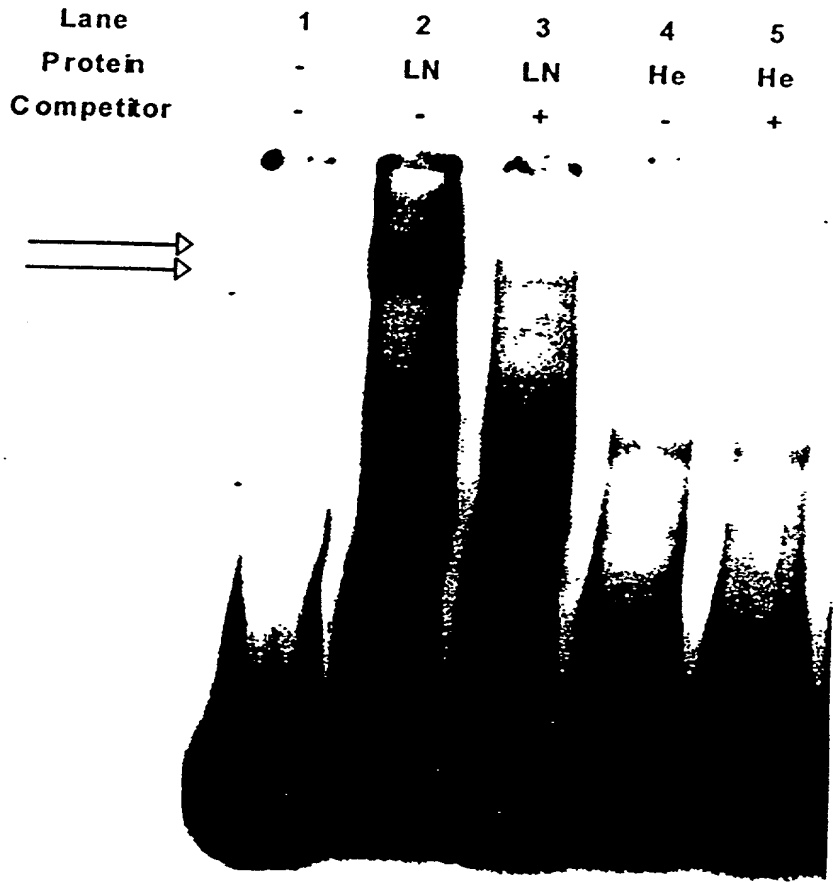


FIGURE 25B

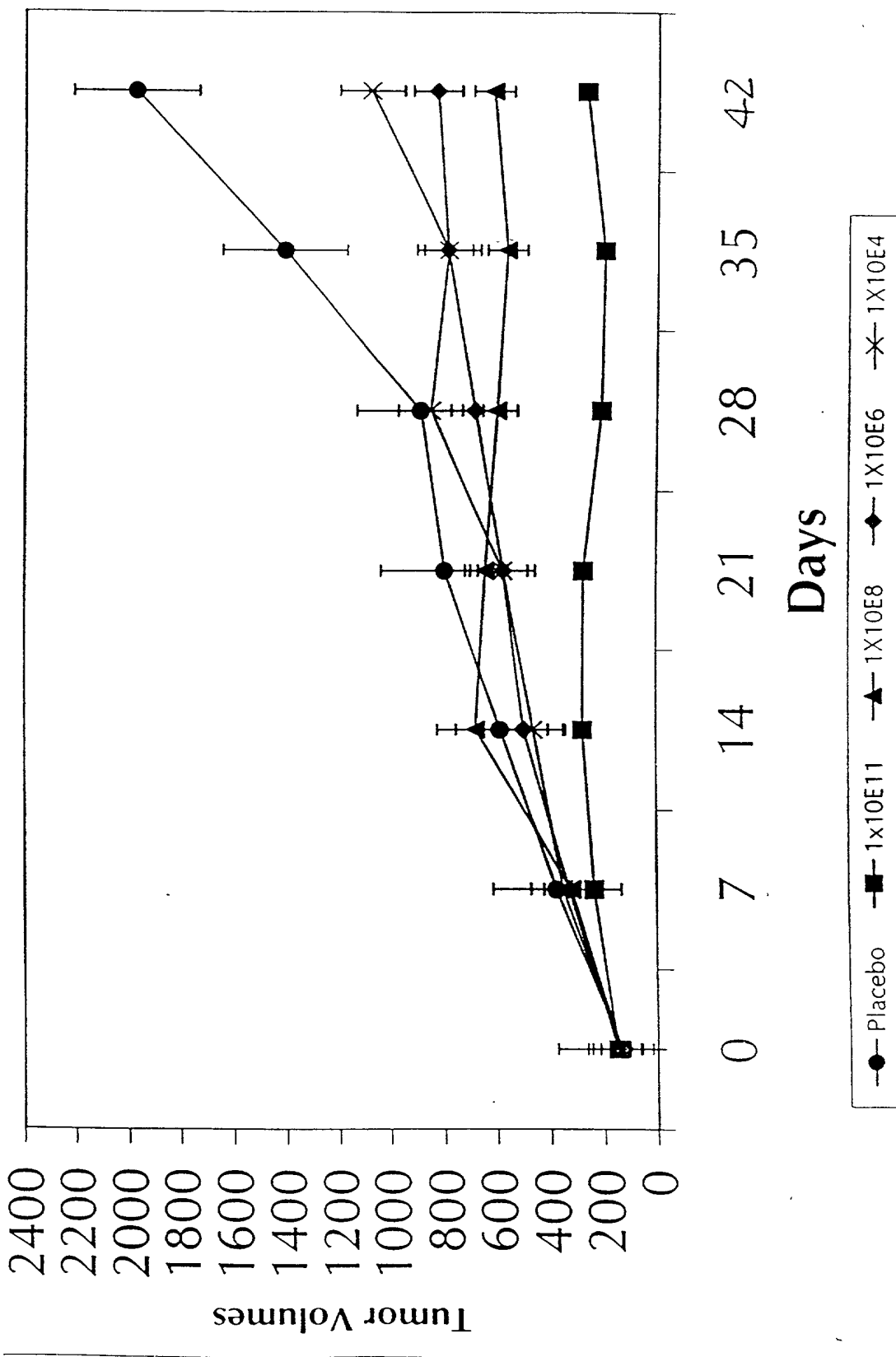


FIGURE 26

FIGURE 26